

GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: October 12, 2002, 13:02:35 : Search time 1833 seconds
(without alignments)
4452.455 Million cell updates/sec

Title: US-09-818-954A-2
Perfect score: 390
Sequence: 1 atgaagctgcctctctt.....ccacgagtgtagaccatc 390

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1797656 seqs, 10463268293 residues
Total number of hits satisfying chosen parameters: 3595312

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: gb_ba:*
2: gb_htg:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_sts:*
12: gb_sy:*
13: gb_un:*
14: gb_vi:*
15: gb_ba:*
16: em_fun:*
17: em_hum:*
18: em_in:*
19: em_mu:*
20: em_om:*
21: em_or:*
22: em_ov:*
23: em_pat:*
24: em_ph:*
25: em_pl:*
26: em_ro:*
27: em_sts:*
28: em_un:*
29: em_vi:*
30: em_htg_hum:*
31: em_htg_inv:*
32: em_htg_other:*
33: em_htgo_inv:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result Query
No. Score Match length DB ID Description

1	390	100.0	390	6	AX259341	AX259341 Sequence
2	390	100.0	917	6	AX201855	AX201855 Sequence
3	378	96.9	693	6	AX193583	AX193583 Sequence
4	300.4	77.0	393	6	AX259351	AX259351 Sequence
5	252	64.6	1045	6	AX201857	AX201857 Sequence
6	204	52.3	122552	9	CNS01DRS	AL118555 Human chr
7	202	51.8	205	6	AX193608	AX193608 Sequence
8	192	49.2	169650	9	CNS00000	AI049871 Human chr
9	156	40.0	2985	6	AX259362	AX259362 Sequence
10	69	17.7	1060	5	AST251658	AX251658 Acipenser
11	66.4	17.0	687	5	SCA310345	AX310345 Scyliorhin
12	61.6	15.8	496	6	108476	108476 Sequence 16
13	61.6	15.8	504	4	CEUHR	Y00518 Dog mRNA fo
14	61.6	15.8	579	4	AY056475	AY056475 Monodelph
15	61	15.6	426	6	108475	108475 Sequence 14
16	60.8	15.6	580	5	AST251656	AJ251656 Acipenser
17	59.2	15.2	558	5	CIGONADB	X61051 C.ideal1a mr
18	59.2	15.2	566	5	AF319960	AF319960 Myiophary
19	58.4	15.0	429	4	AF354938	AF354938 Panthera
20	58.4	15.0	448	5	FUNGPH11	M87015 Fundulus he
21	57.8	14.8	525	6	A06106	A06106 Synthetic p
22	57.8	14.8	629	4	BOVLRBX	M10077 Bovine lutr
23	57.4	14.7	2309	5	AB015596	AB015596 Carassius
24	56.8	14.6	535	5	D88024	D88024 Carassius a
25	56.8	14.6	5651	6	AX211282	AX211282 Sequence
26	56.8	14.6	5651	6	AX349366	E01778 DNA sequence
27	56	14.4	426	5	E01778	AF112192 Ictalurus
28	56	14.4	581	5	AF112192	M27154 Chum salmon
29	56	14.4	661	5	ONHGTTHIB	AF311355 Rana ridi
30	56	14.4	999	5	RI311355	AF112191 Ictalurus
31	56	14.4	1864	4	BOVLRB	D14692 Rainbow tro
32	55.6	14.3	585	4	AF090388	AF090388 Trichosur
33	55.6	14.3	601	4	AF017448	AF017448 Trichosur
34	55.6	14.3	789	5	AF112191	AF112191 Ictalurus
35	55.6	14.3	875	5	ONHTBS	DI4692 Rainbow tro
36	54.8	14.1	595	5	AHA417769	AX17769 Atlantic
37	54.6	14.0	527	5	CHGTTHIB	X91984 C. harengus
38	54.6	14.0	533	4	OLHRS	X52488 Sheep mRNA
39	54.4	13.9	659	5	AB050836	AB050836 Oncorhyn
40	54.4	13.9	1054	9	AF397610	AF397610 Cynoceph
41	54.2	13.9	590	5	MO2GONATIB	L35096 Morone saxa
42	54	13.8	810	5	CCO271632	AJ271632 Conger co
43	54	13.8	866	5	AF060566	AF060566 Salmo sal
44	54	13.8	1066	5	AB016169	AB016169 Anguilla
45	53.6	13.7	426	4	AF448455	AF448455 Alluoropod

ALIGNMENTS

RESULT 1
AX259341 LOCUS 390 bp DNA Linear PAT 26-OCT-2001
DEFINITION Sequence 2 from Patent WO0173034.
AX259341
ACCESSION AX259341
VERSION AX259341.1 GI:16508575
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE
1 (sites)
AUTHORS Paszty,C.J., Gao,J., Danilenko,D.M., Gong,J. and Hill,D.C.
TITLE Beta-like glycoprotein hormone polypeptide and heterodimer
JOURNAL Patent: WO 0173034-A 2 04-OCT-2001;
Amgen Inc. (US)

FEATURES
source location/Qualifiers
1..390
/organism="Homo sapiens"
/db_xref="taxon:9606"

BASE COUNT 69 a 128 c 106 g 87 t
ORIGIN

Query Match 100.0%; Score 390; DB 6; Length 390;
Best Local Similarity 100.0%; Pred. No. 5.5e-87;
Matches 390; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 ATGAAGCTGGGCAATTCCTCTTCTGCGCCCATGGCCCTCTCTTCTGCGCTGCTATGGC 60
|||||
1 ATGAAGCTGGGCAATTCCTCTTCTGCGCCCATGGCCCTCTCTTCTGCGCTGCTATGGC 60
|||||

61 TGTGCTCTCGGTGCTCCAGTGGGAACCTGCGCACCTTTGTGGGCTGTGCCGTGAGGAG 120
|||||
61 TGTGCTCTCGGTGCTCCAGTGGGAACCTGCGCACCTTTGTGGGCTGTGCCGTGAGGAG 120
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121 TTTACTTTCTGCGCAAGACCGAGCTGCAAGGGCTTTGAGATCACACGAGATGCTGC 180
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121 TTTACTTTCTGCGCAAGACCGAGCTGCAAGGGCTTTGAGATCACACGAGATGCTGC 180
|||||

181 TGGGTCGCTGTGAGACCGGGAACCATTTCTGAAACCCCTATTTGAAGCCCAT 240
|||||
181 TGGGTCGCTGTGAGACCGGGAACCATTTCTGAAACCCCTATTTGAAGCCCAT 240
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241 CATGAGTCTGTACTACAGAGACCAACAGGTGACTGTCAAGTCCCAACTGTGCC 300
|||||
241 CATGAGTCTGTACTACAGAGACCAACAGGTGACTGTCAAGTCCCAACTGTGCC 300
|||||

301 CCGGAGTGCAGCCCTTCTACACCTATCCCTGGCCATCCGCTGTGACTGCGGAGCTGC 360
|||||
301 CCGGAGTGCAGCCCTTCTACACCTATCCCTGGCCATCCGCTGTGACTGCGGAGCTGC 360
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361 TCCACTGCCACACGAGAGTGTGAGACCATC 390
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361 TCCACTGCCACACGAGAGTGTGAGACCATC 390
|||||

RESULT 2
AX201855 917 bp DNA Linear PAT 30-AUG-2001
LOCUS
DEFINITION Sequence 1 from Patent WO0153346.
ACCESSION AX201855
VERSION AX201855.1 GI:15391966
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 917)
AUTHORS Mosselman,S. and spek van Der,P.J.
TITLE Human cystine knot polypeptide
JOURNAL Patent: WO 0153346-A 1 26-JUL-2001;
Akzo Nobel N.V. (NL)
FEATURES
source Location/Qualifiers
1. 917
/organism="Homo sapiens"
/db_xref="taxon:9606"
BASE COUNT 222 a 249 c 205 g 241 t
ORIGIN

Query Match 100.0%; Score 390; DB 6; Length 917;
Best Local Similarity 100.0%; Pred. No. 5.1e-87;
Matches 390; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 ATGAAGCTGGGCAATTCCTCTTCTGCGCCCATGGCCCTCTCTTCTGCGCTGCTATGGC 60
|||||
1 ATGAAGCTGGGCAATTCCTCTTCTGCGCCCATGGCCCTCTCTTCTGCGCTGCTATGGC 60
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101 ATGAAGCTGGGCAATTCCTCTTCTGCGCCCATGGCCCTCTCTTCTGCGCTGCTATGGC 160
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101 ATGAAGCTGGGCAATTCCTCTTCTGCGCCCATGGCCCTCTCTTCTGCGCTGCTATGGC 160
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61 TGTGCTCTCGGTGCTCCAGTGGGAACCTGCGCACCTTTGTGGGCTGTGCCGTGAGGAG 120
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61 TGTGCTCTCGGTGCTCCAGTGGGAACCTGCGCACCTTTGTGGGCTGTGCCGTGAGGAG 120
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161 TGTGCTCTCGGTGCTCCAGTGGGAACCTGCGCACCTTTGTGGGCTGTGCCGTGAGGAG 220
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161 TGTGCTCTCGGTGCTCCAGTGGGAACCTGCGCACCTTTGTGGGCTGTGCCGTGAGGAG 220
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121 TTTACTTTCTGCGCAAGACCGAGCTGCAAGGGCTTTGAGATCACACGAGATGCTGC 180
|||||
121 TTTACTTTCTGCGCAAGACCGAGCTGCAAGGGCTTTGAGATCACACGAGATGCTGC 180
|||||

221 TTTACTTTCTGCGCAAGACCGAGCTGCAAGGGCTTTGAGATCACACGAGATGCTGC 280
|||||
221 TTTACTTTCTGCGCAAGACCGAGCTGCAAGGGCTTTGAGATCACACGAGATGCTGC 280
|||||

181 TGGGTCGCTGTGAGACCGGGAACCATTTCTGAAACCCCTATTTGAAGCCCAT 240
|||||
181 TGGGTCGCTGTGAGACCGGGAACCATTTCTGAAACCCCTATTTGAAGCCCAT 240
|||||

|||||
Db 281 TGGGTCGCTGTGAGACCGGGAACCATTTCTGAAACCCCTATTTGAAGCCCAT 340
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Qy 241 CATGAGTCTGTACTACAGAGACCAACAGGTGACTGTCAAGTCCCAACTGTGCC 300
|||||
Db 341 CATGAGTCTGTACTACAGAGACCAACAGGTGACTGTCAAGTCCCAACTGTGCC 400
|||||

Qy 301 CCGGAGTGCAGCCCTTCTACACCTATCCCTGGCCATCCGCTGTGACTGCGGAGCTGC 360
|||||
Db 401 CCGGAGTGCAGCCCTTCTACACCTATCCCTGGCCATCCGCTGTGACTGCGGAGCTGC 460
|||||

Qy 361 TCCACTGCCACACGAGAGTGTGAGACCATC 390
|||||
Db 461 TCCACTGCCACACGAGAGTGTGAGACCATC 490
|||||

RESULT 3
AX193583 693 bp DNA Linear PAT 15-AUG-2001
LOCUS
DEFINITION Sequence 5 from Patent WO0140291.
ACCESSION AX193583
VERSION AX193583.1 GI:15211515
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 693)
AUTHORS Burgess,C.E., Prayaga,S.K., Shinkels,R.A., Rastelli,L.,
Zerhusen,B.D. and Mezes,P.S.
TITLE Proteins and nucleic acids encoding the same
JOURNAL Patent: WO 0140291-A 5 07-JUN-2001;
Curagen Corporation (US)
FEATURES
source Location/Qualifiers
1. 693
/organism="Homo sapiens"
/db_xref="taxon:9606"
BASE COUNT 138 a 197 c 196 g 162 t
ORIGIN

Query Match 96.9%; Score 378; DB 6; Length 693;
Best Local Similarity 100.0%; Pred. No. 5.1e-84;
Matches 378; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 ATGAAGCTGGGCAATTCCTCTTCTGCGCCCATGGCCCTCTCTTCTGCGCTGCTATGGC 60
|||||
1 ATGAAGCTGGGCAATTCCTCTTCTGCGCCCATGGCCCTCTCTTCTGCGCTGCTATGGC 60
|||||

Db 1 ATGAAGCTGGGCAATTCCTCTTCTGCGCCCATGGCCCTCTCTTCTGCGCTGCTATGGC 60
|||||
1 ATGAAGCTGGGCAATTCCTCTTCTGCGCCCATGGCCCTCTCTTCTGCGCTGCTATGGC 60
|||||

Qy 61 TGTGCTCTCGGTGCTCCAGTGGGAACCTGCGCACCTTTGTGGGCTGTGCCGTGAGGAG 120
|||||
Qy 61 TGTGCTCTCGGTGCTCCAGTGGGAACCTGCGCACCTTTGTGGGCTGTGCCGTGAGGAG 120
|||||

Db 61 TGTGCTCTCGGTGCTCCAGTGGGAACCTGCGCACCTTTGTGGGCTGTGCCGTGAGGAG 120
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Db 61 TGTGCTCTCGGTGCTCCAGTGGGAACCTGCGCACCTTTGTGGGCTGTGCCGTGAGGAG 120
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121 TTTACTTTCTGCGCAAGACCGAGCTGCAAGGGCTTTGAGATCACACGAGATGCTGC 180
|||||
121 TTTACTTTCTGCGCAAGACCGAGCTGCAAGGGCTTTGAGATCACACGAGATGCTGC 180
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Db 121 TTTACTTTCTGCGCAAGACCGAGCTGCAAGGGCTTTGAGATCACACGAGATGCTGC 180
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Db 121 TTTACTTTCTGCGCAAGACCGAGCTGCAAGGGCTTTGAGATCACACGAGATGCTGC 180
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Qy 181 TGGGTCGCTGTGAGACCGGGAACCATTTCTGAAACCCCTATTTGAAGCCCAT 240
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Qy 181 TGGGTCGCTGTGAGACCGGGAACCATTTCTGAAACCCCTATTTGAAGCCCAT 240
|||||

Db 181 TGGGTCGCTGTGAGACCGGGAACCATTTCTGAAACCCCTATTTGAAGCCCAT 240
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Db 181 TGGGTCGCTGTGAGACCGGGAACCATTTCTGAAACCCCTATTTGAAGCCCAT 240
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241 CATGAGTCTGTACTACAGAGACCAACAGGTGACTGTCAAGTCCCAACTGTGCC 300
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241 CATGAGTCTGTACTACAGAGACCAACAGGTGACTGTCAAGTCCCAACTGTGCC 300
|||||

Qy 301 CCGGAGTGCAGCCCTTCTACACCTATCCCTGGCCATCCGCTGTGACTGCGGAGCTGC 360
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Db 301 CCGGAGTGCAGCCCTTCTACACCTATCCCTGGCCATCCGCTGTGACTGCGGAGCTGC 360
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Db 301 CCGGAGTGCAGCCCTTCTACACCTATCCCTGGCCATCCGCTGTGACTGCGGAGCTGC 360
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Qy 361 TCCACTGCCACACGAGAG 378
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Qy 361 TCCACTGCCACACGAGAG 378
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Db 361 TCCACTGCCACACGAGAG 378
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Db 361 TCCACTGCCACACGAGAG 378
|||||

[illegible]

Query Match	64.6%	Score 252;	DB 6;	Length 1045;
Best Local Similarity	75.3%	Pred. No. 1.2e-52;		
Matches 390;	Conservative	0;	Mismatches 0;	Indels 128; Gaps 1;
1	ATGAAGCTGGGATTCCTCTTCCTTTGGCCCATATGGCCCTCTCTCTGCTGGCGATATGGC	60		
Db	101 ATGAAGCTGGGATTCCTCTTCCTTTGGCCCATATGGCCCTCTCTCTGCTGGCGATATGGC	160		
QY	61 TGTGTCTCTGGGTGCTCCAGTGGGAACCTGCGACCTTTTGGGCTGTGCCGTAGGGAG	120		
Db	161 TGTGTCTCTGGGTGCTCCAGTGGGAACCTGCGACCTTTTGGGCTGTGCCGTAGGGAG	220		
QY	121 TTTACTTTCTGGCCCAAGAAGCGACGGCGCTTGGGATTCACACAGGATGCCCTGC	180		
Db	221 TTTACTTTCTGGCCCAAGAAGCGACGGCGCTTGGGATTCACACAGGATGCCCTGC	280		
QY	181 TGGGGTCCGCTGGAGACCTGGGAG-----	204		
Db	281 TGGGGTCCGCTGGAGACCTGGGAGCTTTTGTCAAGATGTCTGTTATGAACAAGCATTC	340		
QY	205 -----	204		
Db	341 ATACATTTTGTGTGTGTTACTGGATGAGACCTCCCTCTGAGACTGTAGATCCTCCAGCCT	400		
QY	205 -----AAACCATTCTGCAACCCCTTATTTG	232		
Db	401 AATGGAAGGCATTTAGATACACACTTGCACATTAACCCATTCTGGAMACCCCTTATTTG	460		
QY	233 AAGCCATCATGATGATCTGTACTACCAAGAGAACCAAGGTGACTGCAAGCTGCCCA	292		
Db	461 AAGCCATCATGATGATCTGTACTACCAAGAGAACCAAGGTGACTGCAAGCTGCCCA	520		
QY	293 ACTGTGCCCGGGAGATCGACCCCTTCTACACTATCCCGTGGCCATCCGCTGTGACTCG	352		
Db	521 ACTGTGCCCGGGAGATCGACCCCTTCTACACTATCCCGTGGCCATCCGCTGTGACTCG	580		
QY	353 GAGCCTGCTCCACTGCCACACGAGGTGTGAGACCATC	390		
Db	581 GAGCCTGCTCCACTGCCACACGAGGTGTGAGACCATC	618		

RESULT 6

CNS01DRS

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

REFERENCE

AUTHORS

JOURNAL

COMMENT

1. 1045

/organism="Homo sapiens"

/db_xref="taxon:9606"

BASE COUNT 254 a 279 c 234 g 278 t

ORIGIN

122552 bp DNA linear PRI 26-APR-2001

Human chromosome 14 DNA sequence BAC C-2011M8 of library CalTech-D

from chromosome 14 of Homo sapiens (Human), complete sequence.

AL118555

AL118555.6 GI:13513077

HTG.

human.

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

1 (bases 1 to 122552)

Heilig,R., Petit,J.L., Vico,V., Dasilva,C., Robert,C., Wincker,P.,

Brothier,P., Catolico,L., Babe,V., Pelletier,E., Artiguenave,F.,

Ley,M., Eckenberg,R., Bruns,T., debernardinis,V., Crnaud,C.,

Gyapay,G., Saurin,W. and Weissenbach,J.

Sequencing of the human chromosome 14

Unpublished

2 (bases 1 to 122552)

Genoscope.

Direct Submission

Submitted (26-APR-2001) Genoscope - Centre National de Sequencage :

Bp 191 91006 EVRY cedex - FRANCE (E-mail : sequef@genoscope.cns.fr

- Web : www.genoscope.cns.fr)

On Apr 2, 2001 this sequence version replaced gi:13160378.

Upstream BAC (overlapping the T7 end) : R-1112J20

Downstream BAC (overlapping the SP6 end) : C-2011M8 (AC-AL118555)
----- Summary Statistics -----
Assembly program: Phrap; version 2.0
Quality coverage: 7.69x in Q20 bases; sum-of-coverage

Overall quality chart :
Range : bases

1 - 9 :
10 - 19 :
20 - 29 :
30 - 39 :
40 - 49 :
50 - 59 :
60 - 69 :
70 - 79 :
80 - 89 :
90 - 99 :
112230

Percentage of bases with a quality value >= 40 : 99 %

FEATURES

Location/Qualifiers

1. 169650

/organism="Homo sapiens"

/db_xref="taxon:9606"

/chromosome="14"

/clone="R-696D21"

/clone_id="RPC1-11"

79560. 79769

/note="matching EMBL:G11018

RHdb:RH35164

dbSTS:STS8422

Identified using the e-PCR software (G. Schuler)"

123442. 123577

/note="matching EMBL:N22378

RHdb:RH69284

dbSTS:STS49162

Identified using the e-PCR software (G. Schuler)"

124557. 124675

/note="matching EMBL:HB3430

RHdb:RH77820

dbSTS:STS54562

Identified using the e-PCR software (G. Schuler)"

124823. 124920

/note="matching EMBL:AA011182

RHdb:RH75585

dbSTS:STS52673

Identified using the e-PCR software (G. Schuler)"

125981. 126128

/note="matching EMBL:N67960

RHdb:RH65935

dbSTS:STS45865

Identified using the e-PCR software (G. Schuler)"

52841 a 35988 c 32393 g 48428 t

BASE COUNT

ORIGIN

Query Match 49.2%; Score 192; DB 9; Length 169650;

Best Local Similarity 99.3%; Pred. No. 7.3e-38;

Matches 203; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

1 ATGAAGCTGGCATTCCTCTCTGGCCCGCCATGGCCCTCTCTCTGGCTGATGAGC 60

150808 ATGAAGCTGGCATTCCTCTCTGGCCCGCCATGGCCCTCTCTCTGGCTGATGAGC 150749

61 TGTGTCTCTGCTGCTCCAGTGGGAACCTGTCGACCTTTGTGGCTGTGCGGTGAGGAG 120

150748 TGTGTCTCTGCTGCTCCAGTGGGAACCTGTCGACCTTTGTGGCTGTGCGGTGAGGAG 150689

121 TTTACTTCTCTGCGCCAGACGCTGCGAGGCGCTTGGATGACACGAGATGCTTGC 180

150688 TTTACTTCTCTGCGCCAGACGCTGCGAGGCGCTTGGATGACACGAGATGCTTGC 150630

181 TGGGCTCGCTGTGAGACCTGGAG 204

|||||
Db 150629 TGGGCTCGCTGTGAGACCTGGAG 150606

RESULT 9

AX259362 2985 bp DNA linear PAT 26-OCT-2001

LOCUS

Sequence 23 from Patent WO0173034.

DEFINITION

AX259362

ACCESSION

AX259362.1 GI:16508593

VERSION

AX259362.1

KEYWORDS

house mouse.

SOURCE

Mus musculus

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

REFERENCE

1 (sites)

AUTHORS

Paszty,C.J., Cao,J., Danilenko,D.M., Gong,J. and Hill,D.C.

TITLE

Beta-like glycoprotein hormone polypeptide and heterodimer

JOURNAL

Patent: WO 0173034-A 23 OCT-2001;

FEATURES

Location/Qualifiers

source

1. 2985

/organism="Mus musculus"

/db_xref="taxon:10090"

BASE COUNT

784 a 630 c 761 g 810 t

ORIGIN

Query Match 40.0%; Score 156; DB 6; Length 2985;

Best Local Similarity 85.3%; Pred. No. 9.6e-29;

Matches 174; Conservative 0; Mismatches 30; Indels 0; Gaps 0;

1 ATGAAGCTGGCATTCCTCTCTGGCCCGCCATGGCCCTCTCTCTGGCTGATGAGC 60

150808 ATGAAGCTGGCATTCCTCTCTGGCCCGCCATGGCCCTCTCTCTGGCTGATGAGC 60

61 TGTGTCTCTGCTGCTCCAGTGGGAACCTGTCGACCTTTGTGGCTGTGCGGTGAGGAG 120

150748 TGTGTCTCTGCTGCTCCAGTGGGAACCTGTCGACCTTTGTGGCTGTGCGGTGAGGAG 120

121 TTTACTTCTCTGCGCCAGACGCTGCGAGGCGCTTGGATGACACGAGATGCTTGC 180

150688 TTTACTTCTCTGCGCCAGACGCTGCGAGGCGCTTGGATGACACGAGATGCTTGC 180

181 TGGGCTCGCTGTGAGACCTGGAG 204

181 TGGGCTCGCTGTGAGACCTGGAG 204

RESULT 10

AST251658 1060 bp mRNA linear VRT 03-OCT-2000

LOCUS

Acipenser baerii mRNA for follicle-stimulating hormone (FSH gene).

DEFINITION

Acipenser baerii

ACCESSION

AST251658

VERSION

AST251658.1 GI:8250131

KEYWORDS

follicle-stimulating hormone; FSH gene.

SOURCE

Siberian sturgeon.

ORGANISM

Acipenser baerii

REFERENCE

1 (bases 1 to 1060)

AUTHORS

Querat,B., Selloak,A. and Salmon,C.

TITLE

Phylogenetic analysis of the vertebrate glycoprotein hormone family

JOURNAL

Including new sequences of sturgeon (Acipenser baerii) beta subunits

MEDLINE

of the two gonadotropins and the thyroid-stimulating hormone

REFERENCE

Biol. Reprod. 63 (1), 222-228 (2000)

AUTHORS

Querat,B.

TITLE

Direct Submission

JOURNAL

Submitted (25-NOV-1999) Querat B., Laboratoire de Physiologie

REFERENCE

Generale et Comparee, MNHN-CNRS, 7, rue Cuvier, 75231 Paris cedex

05, FRANCE

Query Match	Best Local Similarity	Score	DB	Length
Matches 145; Conservative	52.5%; Pred. No. 2.3e-06;	66.4;	5;	687;
	0; Mismatches 131; Indels	0;	Gaps	0;
105	CTGTCCCGTGAAGGAGTTTACTTTCCTGTGGCCCAAGAACCCAGGCTGCAGGGCGCTTGGAT	164		
111	CTGCCACCCGACCAATGAGCAATTTCTGCCGAGAAGACGAGTGTCTATTATTTGGCTGAC	170		
165	CACCAAGGATGCTCTGTGGGTCGTGTGAGACTGGGAGAAACCATTTCTGAACCCCC	224		
171	CCTCACTACATTCATATGTCGGTGTACTGTCCCAACAAAGAAATGGTGTACAGAGCC	230		
225	CTATTATTGAAGCCATCATCGAGTCTGTACCTACAGACGACAAACAGGTGACTGTCAA	284		
231	TCTCTTGTCAGTTTACACGACGTGTGATCTTGAAGGATTTGATATGAGACCATGAC	290		
285	GCTGCCAATCTGTGCGCCGGAGGTGACCCCTTCTACACCTATCCCGTGGCCATCCGCTG	344		
291	GCTGCCAGCTGCTGCCAGCGGTGTGACTTCCACCTACACCTAACCCGCTGGCTGACGTG	350		
345	TGACTGCGAGCGTCTCCACTTGCACCCACGACGAGTG	380		
351	TGAATGCAACCTCTGCAGATGTGATACACGATTTG	386		
RESULT 12				
LOCUS	108476	496 bp	Linear	PAT 02-DEC-1994
DEFINITION	Sequence 16 from Patent WO 8607383.			
ACCESSION	108476			
VERSION	108476.1	GI:588819		
KEYWORDS	.			
SOURCE	Unknown.			
ORGANISM	Unknown.			
REFERENCE	1 (bases 1 to 496)			
AUTHORS	Talimadze, K.D. and Fildes, J.C.			
TITLE	AUTONANTIGEN VACCINES			
JOURNAL	Patent: WO 8607383-A 16 18-DEC-1986;			
FEATURES	Location/Qualifiers			
source	1..496			
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BASE COUNT	66 a 191 c 134 g 105 t			
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Query Match	15.8%; Score 61.6; DB 6;	Length 496;		
Best Local Similarity	52.8%; Pred. No. 3.7e-05;			
Matches 133; Conservative	0; Mismatches 119; Indels	0;	Gaps	0;
133	GCCAGAGACCAAGCGCTGAGGGCCTTGGATACACAGGATGCGCTGTGGGTCGCTGT	192		
106	GCTGAGAACGAAGCCTGCGCGGTCTGTATCAACCTTACACACACCATCTGTGCGGGTAC	165		
193	GAGACCTGGGAGAAACCATTTCTGGAACCCCTTATTGAAGCCCATCATCGAGTCTGT	252		
166	TGCCACACATGTGTGAGAGTGTCTGCCACCGCGCTGCACCATGTGTCCACGACGATGTC	225		
253	ACCTTAACGAGACCAACAGGTGACTGTCAAGCTGCCCACTGTGCGCGGAGATCGAC	312		

Db 226 ACCTACATGAGCTGACCTTTCATCCGGCTCCCGAGATCCCGCTGGCGTGAGC 285
QY 313 CCCTTCACACCTATCCGCTGATCGGAGAGCTGCTCAGTCCAGC 372
Db 286 CCATGCTCTCTCCCGGCTCAGCTGCTGCTGGCCCTCCCTCAGCAAC 345
QY 373 ACGAGTGTGAG 384
Db 346 TCCGACTGTGG 357

RESULT 13
LOCUS CFLHBR 504 bp mRNA linear MAM 21-JUN-1995
DEFINITION Dog mRNA for luteinizing hormone (LH) beta subunit.
ACCESSION Y00518.1 GI:907
VERSION Y00518.1
KEYWORDS glycoprotein; hormone; luteinizing hormone.
SOURCE dog.
ORGANISM Canis familiaris
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
REFERENCE 1 (bases 1 to 504)
Wolfe,D.L., Appleby,V.L., Hjerrild,K., Baker,A.R. and Talmadge,K.
Nucleic acid and amino acid sequences of dog beta LH: comparison to
rat, cow and human beta LH
JOURNAL Nucleic Acids Res. 15 (24), 10602 (1987)
MEDLINE 88096605
FEATURES
source Location/Qualifiers
1..504
/organism="Canis familiaris"
/db_xref="taxon:9615"
/clone_lib="(lambda)gt10"
CDS
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/codon_start=3
/product="LH precursor"
/protein_id="CAA68572.1"
/db_xref="GI:860906"
/db_xref="SWISS-PROT:P18842"
/translation="LOGLLILLLSYGCVWASRGPIRLPCRPINATLAENACPVCI
TFTTTCAGYCVSMRVRLPALPPVQPVCTYELHFASTRILPGCPGVDPMVSPVA
LSCRCPPRLNSDCGPPRAOPLACDRPLPLGLFL"
54..416
mat_peptide /product="LH protein"
BASE COUNT 73 a 193 c 133 g 105 t
ORIGIN

Query Match 15.8%; Score 61.6; DB 4; Length 504;
Best Local Similarity 52.8%; Pred. No. 3.7e-05;
Matches 133; Conservative 0; Mismatches 119; Indels 0; Gaps 0;

QY 133 GCCAAGAGCCAGGCTGAGGGGCTTGATGATCACACGATGCTGTGGGGTGGCTGT 192
11 1111 111111 111111 1111 111111 111111 111111
Db 105 GCTGAGAACCAAGACCTCCGCTGTATCATCTTACACACCACTGTCGCGGTAC 164
11 1111 1111 111111 111111 111111 111111 111111
QY 193 GAGACCTGGGAGAAACCATCTTGGAAACCCCTATTTGAAGCCCATCATGAGTGT 252
11 1111 1111 111111 111111 111111 111111 111111
Db 165 TGCCCAAGAGTGTAGACGTGTCACAGCCGCTGACCTGTGCCCCAGCCAGTGTGC 224
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QY 253 ACCTACAAGAGACCAAGAGTGTATGTAAGCTGCCCCAAGTGTGCCCGGAGTGAC 312
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Db 225 ACCTACCATGAGCTGACCTTGTGCTTCATCCGCTCCCGGATCCCGCTGGGTGAG 284
1111 1111 1111111111 111111 111111 111111 111111
QY 313 CCCTTCTACACCTATCCCGTGGCCATCCGCTGTGACTGCGAGCCTGCTCCACTGCCAC 372
1111 1111 1111111111 111111 111111 111111 111111
Db 285 CCCATGCTCTCTCCCGGCTCAGCTGTGCTGTGGCCCTCCGCTCAGCAAC 344
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QY 373 ACGAGTGTGAG 384
111111 111111 111111 111111 111111 111111 111111
Db 345 TCCGACTGTGG 356

RESULT 14

AY056475
LOCUS AY056475 579 bp mRNA linear MAM 16-OCT-2001
DEFINITION Monodelphis domestica luteinizing hormone beta chain precursor,
mRNA, complete cds.
ACCESSION AY056475
VERSION AY056475.1 GI:16186291
KEYWORDS South American short-tailed grey opossum.
SOURCE Monodelphis domestica
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Metatheria; Didelphimorphia; Didelphidae; Monodelphis.
REFERENCE 1 (bases 1 to 579)
Kacsoh,B.
Cloning of a cDNA encoding the luteinizing hormone beta chain
precursor in the marsupial, Monodelphis domestica
JOURNAL Unpublished
AUTHORS Kacsoh,B.
REFERENCE 2 (bases 1 to 579)
Kacsoh,B.
Direct Submission
TITLE Submitted (21-SEP-2001) Division of Basic Medical Sciences, Mercer
University School of Medicine, 1550 College Street, Macon, GA
31207, USA
FEATURES
source Location/Qualifiers
1..579
/organism="Monodelphis domestica"
/db_xref="taxon:13616"
/tissue_type="pituitary gland"
14..439
/note="pituitary gonadotropin; LH-beta precursor,
pre-LH-beta"
/codon_start=1
/product="luteinizing hormone beta chain precursor"
CDS
1..439
/protein_id="A113337.1"
/db_xref="GI:16186292"
/translation="MERYQELTVLLLLLEGGSGAGSFRPLCRPINATLAESDAC
PVCVTFETTCAGYCVSMRVRLPALPPGQVLYRELFESWTRILPGCPGVDPIFS
PVVALSCAGCSRSHSDCGPPRARPLCTRPHLSRL"
BASE COUNT 106 a 216 c 143 g 114 t
ORIGIN

Query Match 15.8%; Score 61.6; DB 4; Length 579;
Best Local Similarity 52.8%; Pred. No. 3.7e-05;
Matches 133; Conservative 0; Mismatches 119; Indels 0; Gaps 0;

QY 133 GCCAAGAGCCAGGCTGAGGGGCTTGATGATCACACGATGCTGTGGGGTGGCTGT 192
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QY 193 GAGACCTGGGAGAAACCATCTTGGAAACCCCTATTTGAAGCCCATCATGAGTGT 252
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QY 253 ACCTACAAGAGACCAAGAGTGTATGTAAGCTGCCCCAAGTGTGCCCGGAGTGAC 312
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Db 248 ACATACAGAGAGCTGACCTTCTCTGATCCGCGCTGATGATGCCCTGAGATGAG 307
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QY 313 CCCTTCTACACCTATCCCGTGGCCATCCGCTGTGACTGCGAGGCTGCTCAGTCCAC 372
1111 1111 1111111111 111111 111111 111111 111111
Db 308 CCCATCTCTCTCCCGGCTCAGCTGTGCTGTGATCTCGCGCTGAGCAAC 367
1111 1111 111111 111111 111111 111111 111111
QY 373 ACGAGTGTGAG 384
111111 111111 111111 111111 111111 111111 111111
Db 368 TCAGACTGTGG 379

RESULT 15
LOCUS 108475 426 bp linear PAT 02-DEC-1994
DEFINITION Sequence 14 from Patent WO 8607383.
ACCESSION 108475
VERSION 108475.1 GI:588818
KEYWORDS Unknown.

ORGANISM	Unknown.
Unclassified.	

REFERENCE 1 (bases 1 to 426)

AUTHORS Talmadge, K. D. and Fiddes, J. C.

TITLE AUTOANTIGEN VACCINES
JOURNAL *Biotechnology*
DATE 1986-DEC-14
DOI 10.1002/biot.280040101

Journal	Patent:	WO 860/383-A 14 18-DEC-1986,	Location/Qualifiers
EATIPRES			

source	location/quarters
1. : 426	

source	1. .426
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/organism="unknown"

RIGIN

Query Match	15.68; Score 61; DB 6; Length 426;
Best Local Similarity	52.68; Pred. NO. 5.3e-05;

Best Local Similarity 52.6%; pred. No. 5.3e-05; Matches 133; Conservatio 0; Mismatches 130

Matches 133; Conservative 0; Mismatches 120; Indels 0; Gaps 0;

[illegible]

Search completed: October 12, 2002, 14:05:09
Job time : 1884 secs